OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/086,510

DATE: 03/19/2002
TIME: 15:08:45

Input Set : A:\50549-20001.20txt.txt
Output Set: N:\CRF3\03192002\J086510.raw

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 4 <110> APPLICANT: Fang-Tseh (Frank) CHANG et al.
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEARL
 7        OYSTER CULTIVATION
 9 <130> FILE REFERENCE: 505493000120
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/086,510
C--> 12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: 60/310,070
15 <151> PRIOR FILING DATE: 2001-08-02
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2050
23 <212> TYPE: DNA
24 <213> ORGANISM: Pinctada margaritifera
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28 acttgactcc tctgcttgtt ctgattccat tatgtcattg tgcctccatg cacaggcatg   120
29 accattatat ggacatggat aaaacctacc gtaatcgatg gggaaactgt cattattcag   180
30 ggguaagtag ctgtgacgcc gggtttagct acaataggga acaaaatgag gaacaatgcc   240
31 acggtccgta tgactggcac actatatcta gttgctttaa ggcatgtgga agtaaagaga   300
32 gacaatcacc aatcaacatt tggtcacata gagccctttt ccgaaaactg ccaagactga   360
33 aattcaagcc acatatgaaa tcattggata cgaaagtgtc aaatcaccaa aatcatgccc   420
34 ctgaattcga ttcagaggac gaaaaacttc atgttaaact gaagaatctt gttgatggac   480
35 attataaatt ccgcaatctc catattcaca ttggcaaaag tagacgaaag ggctccgaac   540
36 acagcgttga cagacatttt acacctatgg aggctcattt agtgttccgt catgatgaga   600
37 aaaaggaaat caaacctcct aggatttggt taggaagaaa tttcagtgga attaatgaat   660
38 ttgttgtcgt tggggttttt ctagaggttg gtgatgaagg atacggtgat gaaccggacg   720
39 acgatgaatg taagcgcata ttaaagggtc attacgatca ttgcgacaac aatggagaca   780
40 acggctacaa ctgtgataac ggcaacaatg gaaacaacgg aaacaatggt aatggtaaca   840
41 acggttataa cggtaacaac ggttataacg gtaataacgg tgacaatggc aacagtggaa   900
42 acaatggtaa tggtaacaac ggttataacg gtaacaacgg ttataacggt aataacggtg   960
43 acaatggcaa cagcggaaac aatggtaatg gtaacaacgg ttataacggt aataacggtg  1020
44 gcaacggaaa caacagaaac aatggcaatg gtaacaacgg aaacaatggt aatgataaca  1080
45 acaatggcaa caacgaaac aatggtaatg gtaacaacgg aaacaatggt aatgataaca  1140
46 acggaaataa tggtaatggt aacaacggaa ataacggtgg caatggcaac aatggaaaca  1200
47 atggtaatgg taacaacgga aataatggta atggtaacaa cggaaataat ggtaatggta  1260
48 acaacggaaa taacggtggc aatggcaaca atggtaatgg taacaatgga aataatggta  1320
49 acggtgacta cggtagtaat ggtaacaatg gtgaaacgg gaacaatggt aataacggtg  1380
50 ataacggtaa tggcgacaat ggttataacg gtgataatgg taacagtgac gggcgactca  1440
51 gacgttggga cttggaaaat gtccgacgca tgcataccga gcgatatcac ttcagcagaa  1500
52 gatgtattgt caaaaaagca aaacgcctca gcaggattct cgaatgcgca tatagacaca  1560
53 aaaaagtcag agaattcaaa aggaatggag aacacaaagg tcttgatgtt gaaattacac  1620
54 cggaaatggt tttaccgcca ataaagtaca gacaatacta tacctatgaa ggatcattga  1680
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55 caacccctcc ttgcgatgag accgtccttt gggttgtaga aaaatgccac gtgcaagtat    1740
56 ccagaagggt gcttgatgca ttgcggaacg ttgaaggata tgaggatggt accacgctga    1800
57 gcaagtatgg aactagacgt cccacacaga gaaacataaa acctttaact gtgtacaaaa    1860
58 acttcatatg atcgaactca ttttctgttc cagtctcgtt aaggaacaaa tgtaaataat    1920
59 gtcacgattc gcacaatgta caatatatct gtttctgcac atcatatgaa gcatactcta    1980
60 atgtaaaact gttaaaaatg atgcaataaa tatgtttttt taaaaaaaaa aaaaaaaaa     2040
                                                                        2050
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63 <210> SEQ ID NO: 2
64 <211> LENGTH: 1811
65 <212> TYPE: DNA
66 <213> ORGANISM: Pinctada maxima

68 <400> SEQUENCE: 2
69 aatgtggaga atgacgacgc ttcttcactt gactgctctg cttgttctga ttccattatg      60
70 tcattgcgcc tccatgcaca ggcatgacca ttatatggac atggatcaaa cctaccctaa     120
71 tggattggga tactgtgaac cttcaggtga aagcagctgt aaagccggat ttagctacaa     180
72 tagagacata tgccaaggtc cgtatcattg gcacactata tctagttgct ataaggcatg     240
73 tggacataaa aggagacaat caccaatcaa catttggtca cataaagctg tattcttacc     300
74 ttatctgcca agactgaaat tcaagccaca tatgaagtca ttggatacgg acgtgacaaa     360
75 tcaccaaaat cgtgcccctg aattcgagcc ggaggacgga gataagcttc atgtgaaact     420
76 aaagaatctt gttgatggac attataaatt tcacaatctc catattcaca acggcaaaag     480
77 tagacgaaag ggctcggaac acagcgtgaa cagacatttt acgcccatgg aggctcattt     540
78 ggtgttccat catgatgata aaaaggaaat caaacctcca agggttaagt tagggggagt     600
79 gtacgctggt cgtaacaaat ttgttgtcgt tggagtcttt ctagaggtgg gtgatgaagg     660
80 atacggtgat gaaccggacg acgatgaatg taagcgcata ttaaagggtc attgcgagaa     720
81 caatggggac aatggtaaca actgtgataa cggcaacaat ggtaacaacg acaacaatgg     780
82 taacaacgga aacaatggta atggtaacaa cggttataac ggtaataacg gtgacaatgg     840
83 aaacaatggc aatggtaatg gtaacaacgg ttataacggt aataacggtt acaatggcaa     900
84 caacggaaac aatggtaatg gtaacaatga caataatggt aacgataaca acggaaataa     960
85 cggtggcaat ggtaacaacg gaaacaatgg taatggtaac aatggaaata atggtaatgg    1020
86 taataacgga aataacggtg gcaatggcaa caacggaaac aatggtaata gtaacaacgg    1080
87 aaataatggt aatggtaaca acggaaataa cggtggcaat ggcaacaacg gaaacaatgg    1140
88 taatggtaac aatgaaaata atggtaacgg tagtaatggt aacaatggtg gaaacggcaa    1200
89 caatggtaat aacggtgata acggtaatgg cgacaatggt tataacggtg ataatggtaa    1260
90 cagtgacggg cgactcagac gctgggattt ggcaaatgtc cgacgcatgc acgccgagcg    1320
91 atatcacttt agcggaggat gtatcgtcaa aaaagctaaa cgcctcagca ggattcttga    1380
92 atgcgcatat agacacaaaa aagtcagaga attcaaaagg aatggagaag aaaaaggtct    1440
93 tgatgttgat attacaccgg aaatggtttt accgccaatg aaatacagac attactatac    1500
94 ttatgaagga tctttgacaa cccctccttg caatgagacc gtcctttggg ttgttgaaaa    1560
95 atgccacgtg caagtatcca gaagggtgct tgatgcattg cggaacgtcg aaggatatga    1620
96 agatggtacc acgctgagca gtatggaac cagacgtccc acacaagaa acaagcatcc       1680
97 tctacgtgtg tacaaaaact ccatataatg atcatggcga gagaatgacg acgcttcttc    1740
98 acttgactgc tctgcctcct cccccacccc cccccggcc atatggccac tctgcgttga      1800
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101 <210> SEQ ID NO: 3
102 <211> LENGTH: 2363
103 <212> TYPE: DNA
104 <213> ORGANISM: Pinctada fucata

106 <400> SEQUENCE: 3
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108 ctgtgttatg gcgcctccat gtttaaacat gaccactaca tggacaatgg tgtgaggtat   120
109 cctaatggtg acggaatctg taaacaattg aatgaaacca aatgtgatgc agggtttagc   180
110 tatgatagga gtatatgtga aggtcctcat tattggcaca ccatatcgaa atgcttcatt   240
111 gcatgtggaa ttggacagag acaatctcca atcaacatcg tttcttatga tgctaaattt   300
112 cgtcagcgtt tgccaaaatt gaaattcaag ccacatatgg agaaattaaa aacagaagtg   360
113 accaatcatc agaaccgagc tccagagttc gagccagagg atggggaaaa tctgtacgtg   420
114 aagctaaata acctagtgga cggtcattat aaattccata atcttcacgt tcataatggt   480
115 agaaccagac gtaagggatc agaacacagt gttaacggtc gtttcacacc tatggaggct   540
116 catttggttt tccatcatga tgatcaaaca cactttgaac ctacacgcac taagctggga   600
117 ggagcattcc ctggtcataa cgattttgtc gtcgttggag tttttcttga ggtcggagat   660
118 gacggctttg gcgacgaacc ggatgacgaa gaatgtaaac acatcttaaa gggacatcac   720
119 cctgataata acgagaacgg caatggagac aatggcaata acggctacaa tggggacaac   780
120 ggtaacaatg gtgacaacgg caataacagc tacaatgggg acaacggtaa caatggtgtc   840
121 aacggcaata acggctacaa tggggacaac ggtaacaatg gagacaacgg caataacggc   900
122 tacaatgggg acaacggtaa caatggtgac aacggcaata acggtgaaaa cggcaataac   960
123 ggtgaaaacg gcaataacgg tgaaaatggt cacaaacacg gatgtcgggt aaagaaagca  1020
124 aagcatctca gtaggatcct ggaatgtgct tatagaaacg ataaggtcag agagttcaag  1080
125 aaagttggag aagaggaagg gttagatgtt catctaacac cggagatggc tttgccgcca  1140
126 ctgaagtaca gacattacta tacatacgag ggatccctga ccactccccc gtgtacagag  1200
127 tctgtcctct gggttgttca aaaatgccat gtgcaggtgt caagaagggt tcttcatgca  1260
128 ttacgaaatg ttgaaggata taaagatggt accacactaa gaaagtatgg aactagacgt  1320
129 ccaacgcaaa agaataaagt tactgtgtac aaaagcttca aatagttgac atagtttttg  1380
130 ttctttttcct tatagagaca tgtaacacag ccaattatgt ttcatatgta atccatgtaa  1440
131 aatacaggat ctttacataa atattcatgt gaaacaagca cgaacattaa aggactaggt  1500
132 gcgctaaccc cttatatcgg ccctataatt tcgacgagaa atgctttaa taaacaaact  1560
133 attaattata gcttttttgca atgttgaatg tttgagaaaa taccgcatca tatttttag   1620
134 ccctcgtaac gtcacgcgag tgatgtatga tgtcatgttc tgaaagtcat ttgccctgaa  1680
135 tgacgcaaaa caaatgagaa tcatcgtatt ttacatacaa atcttcaaat tcatctgcga  1740
136 ttcaggcctc gaacacgata tttttatgc aaatttaaag gccgatcaaa aatccatcga  1800
137 ttagtacaaa tattatcgtg ggcaattaag gcctggaacg atacttaatt tcataaattt  1860
138 taatcgaaat ttcgctgatt tattgatatt ttcaatgagt ttcaacgttt tagacatttt  1920
139 tttgtaatat tcagtatagg actatgaaat caaaaaaagc tttcctgata tggattcacc  1980
140 atacatttaa catttcaaaa actagaatat tatggatata tgaacaactt tgaaaatggg  2040
141 gccgatatgg caggttaccg aacctacttc tttttatcaa atttttaca tgaaattcat  2100
142 gggaagtttc cgacatcaat ttcatgtgaa ttctatatcg catgaaggtc acaaagaaaa  2160
143 tttcatgtaa aattcatgcg aaggaaattc atgtgaaact catgtgaaat attttttcaca  2220
144 taaatcttaa gtgaaaagta tataaatttc acaactttca tgtgaaattt aagtgatgct  2280
145 cattttgtat ggatttcatg tgaggcataa ttgactgctt gtactatgta attagaacaa  2340
146 aatgtcaaat atttaataaa tga                                          2363
148 <210> SEQ ID NO: 4
149 <211> LENGTH: 611
150 <212> TYPE: PRT
151 <213> ORGANISM: Pinctada margaritifera
153 <400> SEQUENCE: 4
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156 Ile Pro Leu Cys His Cys Ala Ser Met His Arg His Asp His Tyr Met
157            20                  25                  30
158 Asp Met Asp Lys Thr Tyr Arg Asn Arg Trp Gly Asn Cys His Tyr Ser
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159         35
160 Gly Gly Ser Ser Cys Asp Ala Gly Phe Ser Tyr Asn Arg Glu Gln Asn
161    50                          55                60
162 Glu Glu Gln Cys His Gly Pro Tyr Asp Trp His Thr Ile Ser Ser Cys
163 65                       70                75                80
164 Phe Lys Ala Cys Gly Ser Lys Glu Arg Gln Ser Pro Ile Asn Ile Trp
165                    85                90                     95
166 Ser His Arg Ala Leu Phe Arg Lys Leu Pro Arg Leu Lys Phe Lys Pro
167            100                 105                110
168 His Met Lys Ser Leu Asp Thr Lys Val Ser Asn His Gln Asn His Ala
169      115                      120                125
170 Pro Glu Phe Asp Ser Glu Asp Glu Lys Leu His Val Lys Leu Lys Asn
171    130                      135                140
172 Leu Val Asp Gly His Tyr Lys Phe Arg Asn Leu His Ile His Ile Gly
173 145                      150             155                160
174 Lys Ser Arg Arg Lys Gly Ser Glu His Ser Val Asp Arg His Phe Thr
175                    165                170                175
176 Pro Met Glu Ala His Leu Val Phe Arg His Asp Glu Lys Lys Glu Ile
177            180                 185                190
178 Lys Pro Pro Arg Ile Trp Leu Gly Arg Asn Phe Ser Gly Ile Asn Glu
179      195                      200                205
180 Phe Val Val Val Gly Val Phe Leu Glu Val Gly Asp Glu Gly Tyr Gly
181    210                      215                220
182 Asp Glu Pro Asp Asp Asp Glu Cys Lys Arg Ile Leu Lys Gly His Tyr
183 225                      230             235                240
184 Asp His Cys Asp Asn Asn Gly Asp Asn Gly Tyr Asn Cys Asp Asn Gly
185                    245                250                255
186 Asn Asn Gly Asn Asn Gly Asn Asn Gly Asn Gly Asn Asn Gly Tyr Asn
187            260                 265                270
188 Gly Asn Asn Gly Tyr Asn Gly Asn Asn Gly Asp Asn Gly Asn Ser Gly
189      275                      280                285
190 Asn Asn Gly Asn Gly Asn Asn Gly Tyr Asn Gly Asn Asn Gly Tyr Asn
191    290                      295                300
192 Gly Asn Asn Gly Asp Asn Gly Asn Ser Gly Asn Asn Gly Asn Gly Asn
193 305                      310             315                320
194 Asn Gly Tyr Asn Gly Asn Asn Gly Gly Asn Gly Asn Asn Arg Asn Asn
195                    325                330                335
196 Gly Asn Gly Asn Asn Gly Tyr Asn Gly Asn Asn Gly Asp Asn Gly Asn
197            340                 345                350
198 Asn Gly Asn Asn Gly Asn Gly Asn Asn Gly Asn Asn Gly Asn Asp Asn
199      355                      360                365
200 Asn Gly Asn Asn Gly Asn Gly Asn Asn Gly Asn Asn Gly Gly Asn Gly
201    370                      375                380
202 Asn Asn Gly Asn Asn Gly Asn Gly Asn Asn Gly Asn Asn Gly Asn Gly
203 385                      390             395                400
204 Asn Asn Gly Asn Asn Gly Asn Gly Asn Asn Gly Asn Asn Gly Gly Asn
205                    405                410                415
206 Gly Asn Asn Gly Asn Gly Asn Asn Gly Asn Asn Gly Asn Gly Asp Tyr
207      420                      425                430
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208 Gly Ser Asn Gly Asn Asn Gly Gly Asn Gly Asn Asn Gly Asn Asn Gly
209             435                 440                 445
210 Asp Asn Gly Asn Gly Asp Asn Gly Tyr Asn Gly Asp Asn Gly Asn Ser
211         450                 455                 460
212 Asp Gly Arg Leu Arg Arg Trp Asp Leu Glu Asn Val Arg Arg Met His
213 465                 470                 475                 480
214 Thr Glu Arg Tyr His Phe Ser Arg Arg Cys Ile Val Lys Lys Ala Lys
215                 485                 490                 495
216 Arg Leu Ser Arg Ile Leu Glu Cys Ala Tyr Arg His Lys Lys Val Arg
217             500                 505                 510
218 Glu Phe Lys Arg Asn Gly Glu His Lys Gly Leu Asp Val Glu Ile Thr
219         515                 520                 525
220 Pro Glu Met Val Leu Pro Pro Ile Lys Tyr Arg Gln Tyr Tyr Thr Tyr
221     530                 535                 540
222 Glu Gly Ser Leu Thr Thr Pro Pro Cys Asp Glu Thr Val Leu Trp Val
223 545                 550                 555                 560
224 Val Glu Lys Cys His Val Gln Val Ser Arg Arg Val Leu Asp Ala Leu
225                 565                 570                 575
226 Arg Asn Val Glu Gly Tyr Glu Asp Gly Thr Thr Leu Ser Lys Tyr Gly
227             580                 585                 590
228 Thr Arg Arg Pro Thr Gln Arg Asn Ile Lys Pro Leu Thr Val Tyr Lys
229         595                 600                 605
230 Asn Phe Ile
231     610
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 568
235 <212> TYPE: PRT
236 <213> ORGANISM: Pinctada maxima
238 <400> SEQUENCE: 5
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241 Ile Pro Leu Cys His Cys Ala Ser Met His Arg His Asp His Tyr Met
242             20                  25                  30
243 Asp Met Asp Gln Thr Tyr Pro Asn Gly Leu Gly Tyr Cys Glu Pro Ser
244         35                  40                  45
245 Gly Glu Ser Ser Cys Lys Ala Gly Phe Ser Tyr Asn Arg Asp Ile Cys
246     50                  55                  60
247 Gln Gly Pro Tyr His Trp His Thr Ile Ser Ser Cys Tyr Lys Ala Cys
248 65                  70                  75                  80
249 Gly His Lys Arg Arg Gln Ser Pro Ile Asn Ile Trp Ser His Lys Ala
250                 85                  90                  95
251 Val Phe Leu Pro Tyr Leu Pro Arg Leu Lys Phe Lys Pro His Met Lys
252             100                 105                 110
253 Ser Leu Asp Thr Asp Val Thr Asn His Gln Asn Arg Ala Pro Glu Phe
254         115                 120                 125
255 Glu Pro Glu Asp Gly Asp Lys Leu His Val Lys Leu Lys Asn Leu Val
256     130                 135                 140
257 Asp Gly His Tyr Lys Phe His Asn Leu His Ile His Asn Gly Lys Ser
258 145                 150                 155                 160
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VERIFICATION SUMMARY   DATE: 03/19/2002
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         Input Set : **A:\50549-20001.20txt.txt**
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date